

RAW SEQUENCE LISTING

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Application Serial Number: 10/550,410
Source: IFWP
Date Processed by STIC: 1/9/07

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IFWP

RAW SEQUENCE LISTING

DATE: 01/09/2007

PATENT APPLICATION: US/10/550,410

TIME: 09:35:43

Input Set : A:\3022-109.ST25.txt

Output Set: N:\CRF4\01092007\J550410.raw

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3 <110> APPLICANT: Burnie, James
4   Matthews, Ruth C.
6 <120> TITLE OF INVENTION: Treatment of Infection Due to Clostridium Difficile
8 <130> FILE REFERENCE: 3022-109
10 <140> CURRENT APPLICATION NUMBER: 10/550,410
11 <141> CURRENT FILING DATE: 2005-09-23
13 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/001383
14 <151> PRIOR FILING DATE: 2004-03-25
16 <150> PRIOR APPLICATION NUMBER: GB0306782.4
17 <151> PRIOR FILING DATE: 2003-03-25
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 975
25 <212> TYPE: DNA
26 <213> ORGANISM: Clostridium difficile
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (40)..(972)
33 <400> SEQUENCE: 1
34 attaccataa taatttaata attacaggag ggtattgat atg aaa ata cta gta          54
35                                     Met Lys Ile Leu Val
36                                     1       5
38 ttt gga gca cgc gat tat gaa gaa cca gta ata aaa aaa tgg tct gaa          102
39 Phe Gly Ala Arg Asp Tyr Glu Glu Pro Val Ile Lys Lys Trp Ser Glu
40       10       15       20
42 gaa cat aag gat gtt caa gtg gat att tat cct gaa aac atg act gaa          150
43 Glu His Lys Asp Val Gln Val Asp Ile Tyr Pro Glu Asn Met Thr Glu
44       25       30       35
46 gaa aat gta gtt aaa gct aaa ggg tat gat ggt ata tct ata caa caa          198
47 Glu Asn Val Val Lys Ala Lys Gly Tyr Asp Gly Ile Ser Ile Gln Gln
48       40       45       50
50 act aac tat ata gat aat cct tat att tat gaa act tta aaa gat gct          246
51 Thr Asn Tyr Ile Asp Asn Pro Tyr Ile Tyr Glu Thr Leu Lys Asp Ala
52       55       60       65
54 ggg gtt aaa gtt ata gct tca aga act gca ggg gtt gac atg ata cat          294
55 Gly Val Lys Val Ile Ala Ser Arg Thr Ala Gly Val Asp Met Ile His
56 70       75       80       85
58 ttt gat tta gtt aat gaa aat gga ctt atc gtt aca aac gtt cct gct          342
59 Phe Asp Leu Val Asn Glu Asn Gly Leu Ile Val Thr Asn Val Pro Ala
60       90       95       100
62 tat tca cct aat gca ata gct gaa tta gct gtt act caa gct atg aac          390
63 Tyr Ser Pro Asn Ala Ile Ala Glu Leu Ala Val Thr Gln Ala Met Asn

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64          105          110          115
66 ctt tta aga aag act cct cta gta aag aaa aaa gtc tgt gaa ggt gat      438
67 Leu Leu Arg Lys Thr Pro Leu Val Lys Lys Lys Val Cys Glu Gly Asp
68          120          125          130
70 tac cgt tgg ata gct gaa ctt ctt gga aca gaa gtt aga tct att aca      486
71 Tyr Arg Trp Ile Ala Glu Leu Leu Gly Thr Glu Val Arg Ser Ile Thr
72          135          140          145
74 gtt ggt gtt ata ggt aca gga aaa ata ggt gct act tct gca aaa tta      534
75 Val Gly Val Ile Gly Thr Gly Lys Ile Gly Ala Thr Ser Ala Lys Leu
76 150          155          160          165
78 ttc aaa ggc cta gga gct aat gta att gca tat gac caa tat cca aat      582
79 Phe Lys Gly Leu Gly Ala Asn Val Ile Ala Tyr Asp Gln Tyr Pro Asn
80          170          175          180
82 agt gat tta aac gat ata tta act tac aaa gat tct tta gaa gac ctt      630
83 Ser Asp Leu Asn Asp Ile Leu Thr Tyr Lys Asp Ser Leu Glu Asp Leu
84          185          190          195
86 cta aaa gaa gct gac gtt ata aca tta cat act cct tta ctt gaa gga      678
87 Leu Lys Glu Ala Asp Val Ile Thr Leu His Thr Pro Leu Leu Glu Gly
88          200          205          210
90 aca aaa cat atg ata aat aaa gat act cta gct ata atg aag gat gga      726
91 Thr Lys His Met Ile Asn Lys Asp Thr Leu Ala Ile Met Lys Asp Gly
92          215          220          225
94 gct tac ata gta aat act gcc cgt ggt ggt tta att gat aca ggg gat      774
95 Ala Tyr Ile Val Asn Thr Ala Arg Gly Gly Leu Ile Asp Thr Gly Asp
96 230          235          240          245
98 tta ata gaa gca cta gac tca gga aaa att aga gct gct gcc ctt gat      822
99 Leu Ile Glu Ala Leu Asp Ser Gly Lys Ile Arg Ala Ala Ala Leu Asp
100          250          255          260
102 aca ttt gaa act gaa gga ttg ttc tta aac aaa aaa atg aat cct gga      870
103 Thr Phe Glu Thr Glu Gly Leu Phe Leu Asn Lys Lys Met Asn Pro Gly
104          265          270          275
106 gaa tta act gac cca gaa ata aat aaa ctt ctt tct atg gaa caa gtt      918
107 Glu Leu Thr Asp Pro Glu Ile Asn Lys Leu Leu Ser Met Glu Gln Val
108          280          285          290
110 ata ttc act cat cat ctt ggt ttc ttc act agt aca gcg att gaa aat      966
111 Ile Phe Thr His His Leu Gly Phe Phe Thr Ser Thr Ala Ile Glu Asn
112          295          300          305
114 ata gtt taa      975
115 Ile Val
116 310
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 311
121 <212> TYPE: PRT
122 <213> ORGANISM: Clostridium difficile
124 <400> SEQUENCE: 2
126 Met Lys Ile Leu Val Phe Gly Ala Arg Asp Tyr Glu Glu Pro Val Ile
127 1          5          10          15
130 Lys Lys Trp Ser Glu Glu His Lys Asp Val Gln Val Asp Ile Tyr Pro
131          20          25          30

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134 Glu Asn Met Thr Glu Glu Asn Val Val Lys Ala Lys Gly Tyr Asp Gly
135           35                40                45
138 Ile Ser Ile Gln Gln Thr Asn Tyr Ile Asp Asn Pro Tyr Ile Tyr Glu
139           50                55                60
142 Thr Leu Lys Asp Ala Gly Val Lys Val Ile Ala Ser Arg Thr Ala Gly
143 65           70                75                80
146 Val Asp Met Ile His Phe Asp Leu Val Asn Glu Asn Gly Leu Ile Val
147           85                90                95
150 Thr Asn Val Pro Ala Tyr Ser Pro Asn Ala Ile Ala Glu Leu Ala Val
151           100               105               110
154 Thr Gln Ala Met Asn Leu Leu Arg Lys Thr Pro Leu Val Lys Lys Lys
155           115               120               125
158 Val Cys Glu Gly Asp Tyr Arg Trp Ile Ala Glu Leu Leu Gly Thr Glu
159           130               135               140
162 Val Arg Ser Ile Thr Val Gly Val Ile Gly Thr Gly Lys Ile Gly Ala
163 145           150               155               160
166 Thr Ser Ala Lys Leu Phe Lys Gly Leu Gly Ala Asn Val Ile Ala Tyr
167           165               170               175
170 Asp Gln Tyr Pro Asn Ser Asp Leu Asn Asp Ile Leu Thr Tyr Lys Asp
171           180               185               190
174 Ser Leu Glu Asp Leu Leu Lys Glu Ala Asp Val Ile Thr Leu His Thr
175           195               200               205
178 Pro Leu Leu Glu Gly Thr Lys His Met Ile Asn Lys Asp Thr Leu Ala
179           210               215               220
182 Ile Met Lys Asp Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Gly Leu
183 225           230               235               240
186 Ile Asp Thr Gly Asp Leu Ile Glu Ala Leu Asp Ser Gly Lys Ile Arg
187           245               250               255
190 Ala Ala Ala Leu Asp Thr Phe Glu Thr Glu Gly Leu Phe Leu Asn Lys
191           260               265               270
194 Lys Met Asn Pro Gly Glu Leu Thr Asp Pro Glu Ile Asn Lys Leu Leu
195           275               280               285
198 Ser Met Glu Gln Val Ile Phe Thr His His Leu Gly Phe Phe Thr Ser
199           290               295               300
202 Thr Ala Ile Glu Asn Ile Val
203 305           310

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206 <210> SEQ ID NO: 3

207 <211> LENGTH: 20

208 <212> TYPE: DNA

209 <213> ORGANISM: Clostridium difficile

211 <400> SEQUENCE: 3

212 atgaaaatac tagtatttgg

20

215 <210> SEQ ID NO: 4

216 <211> LENGTH: 21

217 <212> TYPE: DNA

218 <213> ORGANISM: Clostridium difficile

220 <400> SEQUENCE: 4

221 ttaaactata ttttcaatcg c

21

224 <210> SEQ ID NO: 5

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Input Set : A:\3022-109.ST25.txt

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225 <211> LENGTH: 17
226 <212> TYPE: DNA
227 <213> ORGANISM: Clostridium difficile
229 <400> SEQUENCE: 5
230 gttttcccgag tcacgac 17
233 <210> SEQ ID NO: 6
234 <211> LENGTH: 17
235 <212> TYPE: DNA
236 <213> ORGANISM: Clostridium difficile
238 <400> SEQUENCE: 6
239 caggaaacag ctatgac 17
242 <210> SEQ ID NO: 7
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: Clostridium difficile
247 <400> SEQUENCE: 7
248 atgcatagc atttttatcc 20
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 10
253 <212> TYPE: PRT
254 <213> ORGANISM: Clostridium difficile
256 <400> SEQUENCE: 8
258 Met Lys Ile Leu Val Phe Gly Ala Arg Asp
259 1 5 10

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VERIFICATION SUMMARY

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